

## Exhibit A

## **ALIGNMENTS** with DiCunto et al Sequence

In re application of:	Kapeller-Libermann, Rosana				
Application No.:	10/017216	Group No.:	1652		
Filed:	October 23, 2001	Examiner:	Maryam Monshipouri		
For:	13245, A NOVEL HUMAN MYOTONIC DYSTROPHY TYPE PROTEIN				
	KINASE AND USES THERE	FOR			

SEQ ID 1 versus Di Cunto NT seq ALIGN calculates a global alignment of two sequences version 2.0uPlease cite: Myers and Miller, CABIOS (1989) >seq id 1 6574 nt vs. >DiCunto NT SEO 6954 nt scoring matrix: DNA, gap penalties: -16/-4 Global alignment score: 17998 71.3% identity; Dicunt GAGCGGCCGCCGGGCAGGTCTAGAATTCAGCGGCCGCTGAATTCTAGGTGCTGCCGGAG 20 30 40 /tmp/s -----Dicunt ACCTCAGGGCCCCTTAAAGAGGACCCATTCCCCTGTAGACCAGTCTCTGTCCCCTGCAAG DICUNE CTTTACCTGCATTCTTGCCCATGGCGCTTCCCATTTTCTGTGTGATCTTATCTCCCTCAC 150 160 170 130 140 /tmp/s -----DICUNE TGGGCTCTGTATTCTATTCCGTGCCTAACCCAGCGCCTCCTTCTTGTGTCTTTCTCCCTC 280 300 250 260 270 /tmp/s -----DICUNT TCTAGCCTATCTGGTCAGTCAGGCAACCGATCTTCCTCAGGATCATTGATCTCTGTACCT 310 320 330

DiCunt	CCAGGGGCAGTGA 370	AACCTTCCTTTCC 380	CTGGGATAAT 390	CCTCAAGGCT 400	CACTGATCA 410	AACCTT 420
/tmp/s		- <b></b>		<b></b>		
DiCunt	TGGGCTTGGTTC# 430	ACAGGTTAGGTCT 440	ATGTCAGTAC	GCGACATCAG 460	ATATTTGTG 470	TTCGTC 480
/tmp/s		AGAGCCG				
	AGGGTTTTCTAGG	GGAAAAGAGCTG 500	GTAGAATGGA 510	520	530	540
/tmp/s						
	TCTGCTAGTCCAC 550	560	570	580	590	600
/tmp/s						<b></b>
	TGTATGAGTACCT 610	620	630	640	650	660
/tmp/s						
DiCunt	ACCTCCTCATCCT 670		GAGACACGAC' 690	rctgccaagc 700	710	СТТСАА 720
/tmp/s			AGTG			
DiCunt	TGTCAGTACCCGC 730	TTGACTTTCCCC	:::: AGTGTTCCTT 750	CGGCGTTGGC	: ::::: GGAGAGATG 770	
/ tmp / s	30 40 TTCAAATATGGAG		60 TCG			accccc
	TTCAAGTATGGAG TTCAAGTATGGTG 790	::::::::::::::::::::::::::::::::::::::	::: :: :	::: ::: rgcctccgag	CCCATTGCC	:: :::
/tmp/s	90 100 GCCTCCAGGCTGA		120 AGGGGAAACC		140 ACTCAACAG	CAGATG
			::::::::	::: : :::	::::::::	:::::
	850					900
/tmp/s	150 160 TCTCCTCTTTCCC	GAGAAGGGATAT		CTTTGTTCTC		
DiCunt	TCTGCTCTTTCCC 910					
/tmp/s	210 220 CAGCCTGCTCTGA	TGAAGATTAAGC				
DiCunt	CAACCCGCCCTGA			CTTTGTCCAG		
/tmp/s	270 280 ATAGCTGAGTTAC	AGGAGCTCCAGC				
DiCunt	ATAGCCGAGTTGC					
/tmp/s	330 340 GGTTGTGGTCACT	TTGCTGAAGTGC	AGGTGGTAAG			

DiCunt		STCACTTCO 190	GCTGAAGTGC 1100	AGGTGGTTAG 1110		ACCGGGGA 1130	CGTCTA 114
/tmp/s	390 GCTATGAA	400 AGTGATG	410 AAGAAGAAGG	420 CTTTATTGGC		440 GTTTCATT	rttga
-	:: :::::		:::::::::	::::	:::::: :::	:::::::	:::::
DiCunt		AATCATG <i>i</i> .50	AAGAAGAAGG0 1160	CTTTGCTGGC 1170	CCAGGAACAG 1180	GTTTCATT	TTTCGA 120
/tmp/s			470 TTATCTCGAA				
DiCunt	GAGGAGAG	GAACATAT	::::::::::::::::::::::::::::::::::::::	CACGAGTCC	TTGGATCCCC		
/tmn/s	510	520 .caaaaam	530 CACCTTTATC	540	550 ΔΨΔΨΟΔGCCT	560 GGAGGGGA	ጉጥጥርርርጥ
/ Cmp/ S	:::::::	::::::	:::::::	::::	:::::::::::	:::::::	:: ::
DiCunt		CAAAAATI 270	ACCTTTACC 1280			'GGAGGGGA' 1310	132
/tmp/s			590 PATGAGGACCA		AAACCTGATA		
DiCunt	TCGCTTCT	GAACAGAT	TACGAGGACCA	AATTAGATGA	GAGCATGATC		
/tmp/s	630 GAGCTGAT	640 TTTGGCTC	650 GTTCACAGCG		670 GGGATACGTG	680 CATCGAGAG	CATCAA
-	:::::::	:::::::	:: :::::::	: :: : :::	:::::: :::	::::::::	:::::
DiCunt			FTCCACAGCG1	rgcaccagate 1410	GGGATATGTG 1420	1430	CATCAA 144
/tmp/s			710 GTTGACCGCAC	CAGGACACAT	CAAGCTGGTG		
DiCunt	CCCGAGAA	CATCCTCA	TCGACCGGAG	CGGGAGAGAT	CAAGCTGGTG		
/tmp/s			770 AACAAGATGG				
DiCunt	GCTAAGAT	GAATTCAA	::::::::::::::::::::::::::::::::::::::				
/tmp/s	810	820 'TGAAGTGC	830 CTGACTGTGA	840	850 TGGAAAAGGC	860	CCTGGA
_	::::::::	::::::			::: :::	:: ::::::	::::
	ATGGCTCC L560	GGAAGTG1 1570	TTGACCGTGAT 1580	rgaacgagga 1590	CCGAAGGGGC 1600	ACATACGGO 1610	CTTGG
/tmp/s			890 STGGGCGTGA				
DiCunt			TCGGAGTTG				
	L620	1630	1640	1650	1660	1670	
/tmp/s			950 GCCAGAACCTT				
			CCCGGACCT 1700				
/tmp/s			1010 AAAGTGAGCAG				
			1760				CTGTG
	1050	1060 AGAGAGAC	1070	1080	1090	1100	

	GTCCAGAAA 1800		AGTTCGAGG( 1820	GTCTCTGCTGG 1830	CCACCCTTTC 1840	TTTGCCAGAACG 1850
		CAACATTCGTA				1160 AAGTCTGACGAT
		CAACATCCGTA				AAGTCTGACGAT 1910
		CAATTTTGATG				1220 CTCTCCGTGCCA
		CAATTTTGATG				CTCTGTGTGCCA 1970
/tmp/s						1280 TTCGTACAGCAA
						TTCGTACAGCAA 2030
/tmp/s						1340 CTCCCCTGCCAA
DiCunt						CTCCCCTGCCAA 2090
/tmp/s						1400 AGACTCTCAGGA
DiCunt						AGACTCCCAGGA 2150
/tmp/s						1460 GTCAGAGGTGGA
DiCunt						GTCAGAGGTGGA 2210
/tmp/s						1520 GAGATCCCTCCT
DiCunt						GAGATCCCTCCT 2270
/tmp/s						1580 AAGTTTGGAGCA
DiCunt	GGAGCAGG	ACCTTGCTACC 2290	TACATCACA	GAATGCAGTA	GCTTAAAGCG.	AAGTTTGGAGCA
/tmp/s	1590 AGCACGGAT	1600 GGAGGTGTCC	1610 CAGGAGGAT	1620 GACAAAGCAC	1630 IGCAGCTTCT	1640 CCATGATATCAG ::: :: :: :
DiCunt	AGCGCGGAT	GGAGGTGTCC 2350	CAGGAGGATO 2360	SACAAAGCTC' 2370	TGCAGCTTCT 2380	CCACGACATCCG 2390
/tmp/s	1650 AGAGCAGAG	1660 CCGGAAGCTC	1670 CAAGAAATC	1680 AAAGAGCAGG	1690 AGTACCAGGC	1700 TCAAGTGGAAGA
DiCunt	AGAGCAGAG 2400	CCGGAAGCTC 2410	CAGGAGATCA 2420	AAGGAGCAGG 2430	AGTACCAGGC 2440	TCAGGTGGAGGA 2450
/tmp/s						1760 AAGACGGAGTGA
DiCunt						CAGACGCAGCGA 2510
/tmp/s						1820 CAAGCGGAAAGC

DiCunt				CTCGGCTTGCC 2550		TTCAAGCGGAAGGC 2570
/tmp/s	GACAGAAT	GTCAGCATA	AACTGTTGA	1860 AGGCTAAGGAT	CAAGGGAAG	1880 CCTGAAGTGGGAGA
DiCunt	AAACGAAT		AACTGATGA	AGGCTAAGGAC		CCTGAAGTGGGAGA 2630
/tmp/s	ATATGCGA	AACTGGAGA	AGATCAATG		CTCAAAATTC	1940 CAGGAGCTCCAAGA
DiCunt	ATATTCCA	AACTGGAGA	AGATCAATG		CTGAAGATC	ZAGGAGCTCCAGGA 2690
/tmp/s	GAAACTGG	1960 AGAAGGCTG				
DiCunt	GAAGCTGG	AGAAGGCTG	TAAAAGCCA	GCACAGAGGCC 2730		CTGCAGAATATCCG 2750
/tmp/s	CAA	AGGAGCGAG	CCGAGAGGG.	1990 AGCTGGAGAAG	CTGCAGAACO	2010 CGAGAGGATTCTTC
DiCunt	CCAGGCAA	AGGAGCGAG	CAGAGCGGG.		CTACACAACO	CGGGAAGACTCCTC
		TCAGAAAGA	AGCTGGTGG.		CGCCGCCATT	2070 CCTCTGGAGAACAA
DiCunt	CGAGGGCA	TCAAAAAGA	AGCTGGTGG.		CGCCGCCACT	CCCTGGAGAACAA 2870
	GGTAAAGA	GACTAGAGA	CCATGGAGC	2110 GTAGAGAAAAC	AGACTGAAGO	2130 GATGACATCCAGAC
DiCunt	GGTAAAGA	GACTAGAGA	CCATGGAGC		AGACTGAAGO	GATGACATCCAGAC
	AAAATCCC	AACAGATCC	AGCAGATGG		CTGGAGCTCC	2190 GAAGAGAAACATCG
DiCunt	AAAGTCCG	AACAGATCC	AGCAGATGG	CTGATAAAATT 2970	CTGGAGCTG	SAGGAGAAACATCG 2990
	GGAGGCCC	AAGTCTCAG	CCCAGCACC'		CTGAAACAGA	2250 AAAGAGCAGCACTA
DiCunt						AAGGAACAGCACTA 3050
	TGAGGAAA					2310 GCTGACAAGGAGAC
DiCunt						GCCGACAAGGAGAG 3110
	ACTGGAGA	ACATGATGC	AGAGACACG			2370 GGCAAAATTCTCAG
DiCunt	CCTGGAGA	ACATGATGO	AGAGACACG			GGCAAGATCCTCAG 3170
	CGAACAGA		TCAATGCTA'			2430 CTGGAACAGAGGAT
DiCunt		AGGCGATGA	TCAACGCGA'			CTGGAGCAGAGGAT 3230
	TGTGGAAC	TGTCTGAAG	CCAATAAAC		AGCAGTCTT	2490 TTTACCCAAAGGAA
	• • • • •			· · · · · · · · · · · ·		

	CGTGGAG 3240	CTGTCGGAA 3250	GCCAACAAGC 3260	TTGCGGCAAA 3270	CAGCAGTCTC 3280	TTCACCCAGAGGA 3290
			GAGATGATTT			2550 TTTTACCTGGAGA
DiCunt						::::::::::::::::::::::::::::::::::::::
	3300	3310	3320	3330	3340	3350
			GAGGCCCAGA			2610 CTGGAGAAGATCA
DiCunt		GGAAAGCTG				:::::::::: CTGGAGAAGATCA 3410
		GACCACAGT	GACAAGAATC			2670 AGATTGCGGGAGG
DiCunt	:::::: CCACCAA 3420	GATCACAGT	::::::::::::::::::::::::::::::::::::::	GGCTGCTGGA	::::: ::: GCTGGAAACA 3460	:: :::::: AGGCTGAGGGAGG 3470
		GAGCACGAG	GAGCAGAAAC			2730 ACAGAGCTACAGC
DiCunt		GAGCACGAG	GAGCAGAAGC			:: ::::: :::: ACGGAGCTGCAGC 3530
		CAGGAGCGC	GAGTCACAGT			2790 CGGGCGGCCCTGG
DiCunt	GTCCCTG		GAGTCCCAGC	TGACGGCCCT		::::: :: :::: CGGGCAGCGCTGG 3590
28	300	2810	2820	2830	2840	2850
	GAGCCAG	CTTCGCCAG	GCGAAGACAG.	AGCTGGAAGA		GAAGCTGAAGAGG
DiCunt		CTCCGCCAG	GCGAAGACAG.			GAAGCGGAGGAGG 3650
			GCACATAGAG.			2910 GATGCTCTTCGTA
DiCunt	GATCCAG	GCGCTCACG	GCACATCGCG.		GCGCAAATTC	::::: ::::: : GATGCCCTTCGCA 3710
		ACTGTAATC	ACAGACCTGG.		AAACCAGCTG	2970 ACCGAGGACAACG
	CAGCTGC.	ACGGTCATC	ACCGACCTGG.		GAACCAGCTC.	::::::::: ACCGAGGACAACG 3770
	TGAACTC.			TGTCCAAACA	ACTCGATGAG	3030 GCTTCTGGCGCCA
DiCunt	CGAGCTC.		AACTTCTACC			::::: :: :::: GCTTCCGGGGCCA 3830
					TCTCCGCCGG	3090 GAGATCACGGAAC
DiCunt	TGACGAG.					::::::::::::::::::::::::::::::::::::::
	AGAGATG	CAGCTTACC	AGCCAGAAGC.		GGCTCTGAAG.	3150 ACCACGTGCACCA
DiCunt	GGAGATG	CAGCTCACC	AGCCAGAAGC.			:: :: :::::: ACGACATGCACCA 3950
3.1	160	3170	3180	3190	3200	3210

DiCunt		GAGCAGGTC0 3970			CGACGAGCTG 4000	CTGGAGAAGGAGC 4010
	GCAGTGG	GAGGCCTGG	AGGAGCGTCC'		GAAATCCCAG'	TTTGAGTGTCGGG
DiCunt		GAGGCCTGG	CGGAGCGTCC'			:: :::::::::::::::::::::::::::::::::::
	280 TCGAGAG		3300 ATGCTGGACA		3320 GAGCAGGGCG	3330 AGAGCCGATCAGC
DiCunt	TCGAGAG	CTACAGAGG	ATGCTGGACA	CCGAGAAGCA		:: :::::::: AGGGCCGATCAGC 4130
		GAGTCTCGC	CAGGTGGTGG		GAAGGAGCAC	3390 AAGGCTGAGATTC
DiCunt		GAGTCGCGC				::::: :::::: AAGGCCGAGATTC 4190
	CGCTCTG	CAGCAGGCT		AGAAGCTGAA		CTCTCTGACAAGC
DiCunt	TGCTCTG	CAGCAGGCT	CTCAAGGAGC		AGCCGAGAGC(	:: :: :::::: CTGTCGGACAAGC 4250
		CTGGAGAAG	AGCATGCTA'		GAATGCCCGA	3510 AGCTTACAGCAGA
DiCunt		CTGGAGAAG	AGCACGCCA'			::::::::::::::::::::::::::::::::::::::
			GAGCTCAAAC		GGAAGAGCAA	GCCAAATTACAGO
DiCunt	ACTAGAG	ACAGAGCGG(	SAGCTCAAAC		GGAGGAGCAA	::::::::::::::::::::::::::::::::::::::
	GCAGATG	GACCTGCAG	AAAAATCACA'		GACTCAAGGA	3630 CTGCAAGAAGCTO
DiCunt	GCAGATG	GACCTGCAG				::::: :: :: :: :: :: :: :: :: :: :: ::
	AGATCGG	GCTGATCTAG		AAAGAAGTGA	CTTGGAGTAT	CAGCTGGAAAAC
DiCunt						::::::::::::::::::::::::::::::::::::::
	TCAGGTT	CTCTATTCT	CATGAAAAGG'		AGGCACTATT	3750 FCTCAACAAACC
DiCunt	TCAGGTT	CTCTACTCT	CACGAGAAAG'		AGGCACAATC'	::::: :::::: PCTCAGCAAACC# 4550
	ACTCATTO	GATTTTCTG	CAAGCCAAAA		TGCTAAAAAG?	AAAAAGGGTTTA1
DiCunt	ACTCATTO		CAAGCCAAAA'			:::::: \AAAAAGG
				3850 FACCCACACA	GGTTCCTCTG	CAGTACAATGAGO
DiCunt					TTCCTCTG6	::::::::::::::::::::::::::::::::::::::
		GCCCTGGAG		3910 CTCGCTGTGC		3930 GAAGCCCTTCAGA

Dicume	COIIII	5360		5380	ACTTGCAAAT 5390	5400	541
/tmp/s							
DiCunt	CCCAT	ACATCCTGA	AGATGGAGT	CTCACCCACA	CACCACCTGC 5450	TGGCCTGGG	AGAACC
		3420	5430	3440	3430	2400	J=7
/tmp/s							
DiCunt	CTACT				GCGCTGGGTC 5510		GAATCT 553
/tmp/s				4660 <b>-</b> AAAAGC	AGAAGCTGAT	GCTAAACTG	CTTGGA
				::: ::	::::::::: CGAAGCCGAT	::::::	::::::
DiCunt	CGTCG	5540	5550	5560	5570	5580	559
	590 CMCCC				4730 AGACATGAAC		
/ Cmp/s					AGACATGAAC		
DiCunt	CTCTC				TGACATGAAC 5630		CCCTTC. 565
	750				4790 GCTCTACGCC		
/tmp/s					GCTCTACGCC		
DiCunt	TGACC	AGGTGGTGC	TGGTGGGCA	CGGAGGAAGG	CCTCTACGCC 5690	CTGAATGTC	TTGAAA
48	310	4820	4830	4840	4850 CTTCCAAATT	4860	
/ CMp/s					CTTCCAAATT		
DiCunt	CTCCT				CTTCCAAATT 5750		AAGGAC 577
	370 GGAGA	4880			4910 GGCACTGTGT		
-	:::::	:::: ::::	:::::::	: :::::::	::: :::::	:: :::::	:::::
DiCunt					GGCTCTGTGC 5810		
	930 acaca	4940	4950	4960	4970 TGCCCAGCCC		
=	::::	: ::::::	:::: ::::	: :::::::	::::::::	::: ::::	:::::
DiCunt	GGTGA	AGCAGTCCC 5840	TGGCGCAGT 5850	CACACCTGCC 5860	TGCCCAGCCC 5870	GACGTCTCC 5880	CCCAAC. 589
	90	5000	5010				
/tmp/s					GGCAGGCAAG		
DiCunt				ACTTGTTCGC	TGCTGGCAAG 5930		
	)50	5060	5070		5090 TCTCCGCTAC		
	::::	: :: :: :	:::: ::::	::::::::::	::::::::	:: :: :::	:::::
DiCunt	CATCT	GCGCCGCTA 5960			CCTCCGCTAC 5990	AATGACAAC 6000	CTCAGC 601
	l10 ATACT	5120 GCATCCGGA			5150 GCCCTGCAGC		
. •	::::	:::::::::::::::::::::::::::::::::::::::	: ::::: :	:::::::::	::::::::	:::::::	:::::
Dicunt	GTACT				GCCCTGCAGC 6050	6060	TTCACC 607
	170 TTACA	5180 GTATCCTCA	5190				
/tmp/s					CGAAATCGAC		

DiCunt	GAAGTCCCCAG 6800	GCCGAATGCT( 6810				ACTGTTTGA 6850
/tmp/s	5950 AGACAGCAGCA	5960 .GGGGCCGGCT	GCTGCGGGA	GCCGTGAGGA	CCCCGCTGTC	CCAGGTGAA
DiCunt	AGACAGCAGCA	GGGGCCGGCTC 6870	GCCTGCAGGA	GCAGTGAGGA	CCCCACTGTC	CCAGGTTAA
_	CAAGGGAAGAG		CTCTCAAGTT	TTCACGGTTA	ACACTGTCAC	CTATTATGA
DiCunt	CAAGG					TCTG- 6920
/tmp/s	CTGGAATAAAA	6080 AGCTGGACAA	CTGCCAGCT	AACTGGTCAG'	TCCTGAGGAT	CATCCAGCT
DiCunt		:::: GGAC			:: : :: :: PCTTCAGTAT 930	
/tmp/s	GAATGGAGAAA	6140 TCCGGCAGCA	GGTTGAAAAG'	TCTGTTCTGA	GAACAGATTA	TTGCTGAGC
DiCunt			AAG' 6940	TCT		
	AGAGTTCATGT		CGTGGTGACT	TAAAAAATGG	CCTTAAGGCT	GCAGAGCCA
DiCunt		<b>-</b> -				CA
/tmp/s	GCCACCTCTGC	6260 TTACAAAAAG			GTAAGAAACA	
DiCunt	GCCA				:::: GAAA 6950	
/tmp/s	6310 CCTCATCTAGA	6320 AATCAGAAAGO	6330 CTTCTAATTT	6340 CTATAGAAAT	6350 GACACCTCCC	6360 TGGAGCCGA
DiCunt						
	GAGACAATCTG	6380 TTGTTGATTT	rgaaggacag	6400 GCAAGACCAA	6410 CACTGTATTT	6420 AGTTCCATA
DiCunt						
/tmp/s		6440	6450	6460	6470 ACAGATGACT	
_	6430	6440 ACAGGGACAAG	6450 GTGGCTGGCC	6460 TTAAAAACAC	ACAGATGACT	
DiCunt	6430 GCCAGGCCTCA 6490 GTGTGGCCTCA	6440 ACAGGGACAAG  6500 GTCCCTGTTTG	6450 GTGGCTGGCC'  6510 CCCAGAATTT	6460 FTAAAAACACA 	ACAGATGACT  6530 GGAGTTAGCA	GGAAATGAT  6540 TTCATTTT
DiCunt	6430 GCCAGGCCTCA	6440 ACAGGGACAAG  6500 GTCCCTGTTTG	6450 GTGGCTGGCC'  6510 CCCAGAATTT	6460 FTAAAAACACA 	ACAGATGACT  6530 GGAGTTAGCA	GGAAATGAT  6540 TTCATTTT
DiCunt /tmp/s DiCunt	6430 GCCAGGCCTCA 6490 GTGTGGCCTCA	6440 ACAGGGACAAG 6500 GTCCCTGTTTG	6450 GTGGCTGGCC  6510 CCCAGAATTT  6570	6460 ITTAAAAACACA 	ACAGATGACT  6530 GGAGTTAGCA	GGAAATGAT  6540 TTCATTTT

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## SEQ ID 3 versus DiCunto NT Seq

	calculates a glol on 2.0uPlease cit d 3				.989)	
-			61	.59 nt vs.		
>DiCunt	to NT SEQ		6954 nt			
scoring 75.0%	g matrix: DNA, ga identity;	ap penaltie Global		score: 19	433	
/tmp/s						
		20	30	40	50	60
/tmp/s						
	ACCTCAGGGCCCCTTZ 70	80	90	100	110	120
/tmp/s						
		140	150	160	170	180
/tmp/s						
	TTAACTCTCTGTTCCT	200	210	220	230	240
/tmp/s						
DiCunt	TGGGCTCTGTATTCTA 250	ATTCCGTGCCT 260		СТССТТСТТС 280	TGTCTTTCT 290	CCCTC 300
/tmp/s						
DiCunt	TCTAGCCTATCTGGTC			TCAGGATCAT 340	TGATCTCTG 350	TACCT 360
/tmp/s						
DiCunt	CCAGGGGCAGTGAACC 370					
/tmp/s						
DiCunt	TGGGCTTGGTTCACAC	GGTTAGGTCTA 440	TGTCAGTACG 450	CGACATCAGA 460	TATTTGTGT 470	TCGTC 480
/tmp/s						
DiCunt	AGGGTTTTCTAGGGGA 490	AAAAGAGCTGG 500	TAGAATGGAA 510	AAGTGGAGAT 520	TTATTAGGC 530	TGCAG 540
/tmp/s					<b>-</b> -	
DiCunt	TCTGCTAGTCCACCAZ 550	ATGGCTGGTAG 560	TTCTTTTGGA 570	AATGATTTAT 580	TTCCATCCC 590	TTATG 600

						/ CILD/ S
GTCGCC 660			TGTGTCTGTG 630		TGTATGAGTACCT	DiCunt
						/tmp/s
CCTTCAA 720	AGCCCTTCCTGC 710	ACTCTGCCAA 700	GGGAGACACG 690		ACCTCCTCATCCTC	DiCunt
						/tmp/s
TTGAAG	GGCGGAGAGAT	TTCGGCGTTG 760	CCAGTGTTCC 750	TTGACTTTCC 740	TGTCAGTACCCGC	DiCunt
		GGTGCTGCTG		CGCGGAATCC	TTCAAATATGGAG	_
			GCCGGAGGCC		TTCAAGTATGGTG	DiCunt
	ATGACTCAACAC	CCACCTTTA		ATCTGTTCTT	GCCTCCAGGCTGA	
			CCAGGGGAAA		GCCTCCAGGCTAAA	DiCunt
ATGCAGT					30 140 TCTCCTCTTTCCC	
			GCTAGACGCC		TCTGCTCTTTCCCC	DiCunt
CGACACC	240 CGGAAGTATTCO	230 AACTTTGTCC	220 GCACGTGAGC	210 TGAAGATTAA	90. 200 CAGCCTGCTCTGAS	
		AGCTTTGTCC		TGAAGATGAA	CAACCCGCCCTGAS	DiCunt
rcttgta	300 GAAGTCAGAAG1	290 AAGGACTTCG	280 GCCTTCGGCA	270 AGGAGCTCCA	50 260 ATAGCTGAGTTAC	
			GCCGTCGGCG		ATAGCCGAGTTGCC	DiCunt
CATCTAT			340 GCAGGTGGTA		LO 320 GGTTGTGGTCACT	31 /tmp/s
					GGCTGTGGTCACT	
rttgag	420 CAGGTTTCATT	410 GCCCAGGAGC	400 GGCTTTATTG	390 TGAAGAAGAA	70 380 GCTATGAAAGTGA	37 /tmp/s
					GCCATGAAAATCAT	DiCunt
					GAAGAGCGGAACA	43 /tmp/s
					GAGGAGAGGAACAT 1210	DiCunt
					TTTCAGGACAAAA	49 /tmp/s
	::::::::: CCTGGAGGGGAT 1310				TTTCAGGACAAAAA	DiCunt

3440 3450

/tmp/s	5400 5410 5420 5430 5440 5450 CGATCTCAAGTGGAGTCGCTTACCTTTGGCCTTTGCCTACAGAGAACCCTATCTGTTTGT
DiCunt	TGATCTCAAGTGGAGTCGCTTACCTCTGGCCTTCGCCTACAGAGAACCTTATCTGTTTGT 6320 6330 6340 6350 6360 6370
/tmp/s	5460 5470 5480 5490 5500 5510 GACCCACTTCAACTCACTCGAAGTAATTGAGATCCAGGCACGCTCCTCAGCAGGACCCC
DiCunt	GACTCACTTCAACTCCCTGGAAGTCATTGAGATCCAGGCCAGATCCTCACTGGGGAGCCC 6380 6390 6400 6410 6420 6430
/tmp/s	5520 5530 5540 5550 5560 5570 TGCCCGAGCGTACCTGGACATCCCGAACCCGCGCTACCTGGGCCCTGCCATTTCCTCAGG
DiCunt	TGCCCGAGCATATCTGGAAATTCCAAACCCTCGCTACCTGGGCCCTGCGATTTCCTCCGG 6440 6450 6460 6470 6480 6490
/tmp/s	5580 5590 5600 5610 5620 5630 AGCGATTTACTTGGCGTCCTCATACCAGGATAAATTAAGGGTCATTTGCTGCAAGGGAAA
DiCunt	AGCGATTTACCTGGCCTCCTCATACCAGGACAAGTTAAGGGTCATATGCTGCAAAGGAAA 6500 6510 6520 6530 6540 6550
/tmp/s	5640 5650 5660 5670 5680 5690 CCTCGTGAAGGAGTCCGGCACTGAACACCACCGGGGCCCGTCCACCTCCCGCAGCAGCCC
DiCunt	CCTCGTGAAGGAGTCAGGCACTGAGCAGCCCGGGTGCCCTCCACCTCCCGCAGCAGCCC 6560 6570 6580 6590 6600 6610
/tmp/s	5700 5710 5720 5730 5740 5750 CAACAAGCGAGGCCCACCCACGTACAACGAGCACATCACCAAGCGCGTGGCCTCCAGCCC
DiCunt	CAACAAGCGAGGCCCACCAACATACAACGAGCACATCACCAAACGCGTGGCCTCCAGCCC 6620 6630 6640 6650 6660 6670
/tmp/s	5760 5770 5780 5790 5800 5810 AGCGCCGCCGAAGGCCCCACCGCGAGAGCCAAGCACACCCCACCGCTACCGCAA ::::::::::::::::::::::::::::::::
DiCunt	GGCGCCACCGGAAGGCCCCAGCCACCCCGAGAGCCAAGCACACCGCACCGCTACCGAGA 6680 6700 6710 6720 6730
/tmp/s	5820 5830 5840 5850 5860GGGGCGGACCGAGCTGCGCAGGACAGTCTCCTGGCCGCCCCCTGGAGCGAGA ::::::::::::::::::::::::::::::
DiCunt	CAGAGAGGGTCGGACAGACTGCGCAGGGACAAGTCTCCAGGCCGCCCTCTGGAGCGGGA 6740 6750 6760 6770 6780 6790
/tmp/s	5870 5880 5890 5900 5910 5920 GAAGTCCCCCGGCCGGATGCTCAGCACGCGGAGAGAGCGGTCCCCCGGGAGGCTGTTTGA
DiCunt	GAAGTCCCCAGGCCGAATGCTCAGCACTAGGAGAGAGCGGTCCCCAGGGAGACTGTTTGA 6800 6810 6820 6830 6840 6850
/tmp/s	5930 5940 5950 5960 5970 5980 AGACAGCAGCAGGGGCCGGCTGCCGGGGAGCCGTGAGGACCCCGCTGTCCCAGGTGAA
DiCunt	AGACAGCAGCAGGGCCGCCTGCCAGGAGCAGTGAGGACCCCACTGTCCCAGGTTAA 6860 6870 6880 6890 6910
•	5990 6000 6010 6020 6030 6040 CAAGGGAAGAGGCCAGAGTTTTCACGGTTAACACTGTCACCTATTATGA
DiCunt	CAAGGTCTG
-	6050 6060 6070 6080 6090 6100 CTGGAATAAAAAGCTGGACAACCTGCCAGCTAACTGGTCAGTCCTGAGGATCATCCAGCT :::: ::::::::::::::::::::::::::::::::
DiCunt	:::: :::::::::::::::::::::::::::::::::